IN THE CLAIMS

1-30. (Canceled)

31. (Currently Amended) A method of altering the oil composition of a soybean plant cell comprising:

(A) transforming a soybean plant cell with a recombinant nucleic acid molecule which comprises a first set of DNA sequences that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a soybean FAD2 gene and a soybean FATB gene, and a second set of DNA sequences that is capable, when expressed in a host cell, of increasing the endogenous expression of at least a delta-9 desaturase gene; and

(B) growing said soybean plant cell under conditions wherein transcription of said first set of DNA sequences and said second set of DNA sequences is initiated, whereby said oil composition is altered relative to a soybean plant cell with a similar genetic background but lacking the recombinant nucleic acid molecule.

32. (Canceled)

33 . (Previously Presented) The method of claim 31, wherein said cell is present in a multicellular environment.

34. (Previously Presented) The method of claim 33, wherein said cell is present in a transformed plant.

35. (Previously Presented) The method of claim 31, wherein said alteration comprises an increased oleic acid content, a reduced saturated fatty acid content, and a reduced polyunsaturated fatty acid content, relative to a plant cell with a similar genetic background but lacking the recombinant nucleic acid molecule.

36. (Currently Amended) A method of producing a transformed soybean plant having seed with a reduced saturated fatty acid content comprising:

(A) transforming a soybean plant cell with a recombinant nucleic acid molecule which comprises a first set of DNA sequences that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a soybean FAD2 gene and a soybean FATB gene[s], and a second set of DNA sequences that is capable, when expressed in a host cell, of increasing the endogenous expression of at least a delta-9 desaturase gene; and

(B) growing the transformed soybean plant, wherein the transformed soybean plant produces seed with a reduced saturated fatty acid content relative to seed from a soybean plant having a similar genetic background but lacking the recombinant nucleic acid molecule.

37. (Previously Presented) The method of claim 36, wherein said growing step further comprises expressing the first set of DNA sequences and said second set of DNA sequences in a tissue or organ of a plant, wherein said tissue or organ is selected from the group consisting of roots, tubers, stems, leaves, stalks, fruit, berries, nuts, bark, pods, seeds and flowers.

38. (Previously Presented) The method of claim 36, wherein said growing step further comprises expressing the first set of DNA sequences and said second set of DNA sequences in a seed.

39-74. (Canceled)

75. (Previously Presented) The method of claim 31, wherein said first set of DNA sequences that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a FATB gene comprises a FAD2 intron.

76. (Previously Presented) The method of claim 31, wherein said first set of DNA sequences that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a FATB gene comprises a FAD2 intron and a FATB UTR.

77. (Previously Presented) The method of claim 31, wherein said first set of DNA sequences that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a FATB gene comprises a FATB UTR.

78. (Previously Presented) The method of claim 31, wherein said transforming a plant cell with a recombinant nucleic acid molecule comprises cotransforming a first recombinant nucleic acid molecule comprising a DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a second recombinant nucleic acid molecule comprising a DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FATB gene.

79. (Previously Presented) The method of claim 31, wherein said transforming comprises sequentially transforming a first recombinant nucleic acid molecule comprising a DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a second recombinant nucleic acid molecule comprising a DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FATB gene.

80. (Previously Presented) The method of claim 31, wherein said transforming comprises a single transformation of one recombinant nucleic acid molecule comprising a first DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a second DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FATB gene.

81. (Previously Presented) The method of claim 31, wherein said first set of DNA sequences comprises a single contiguous FAD2 sequence or a combination of FAD2 sequences.

82. (Previously Presented) The method of claim 31, wherein said first set of DNA sequences comprises a single contiguous FATB sequence or a combination of FATB sequences.

83. (Previously Presented) The method of claim 31, wherein said first set and second set of DNA sequences are located on one or more T-DNA regions, wherein each of said T-DNA region is flanked by a right border and a left border.

84. (Previously Presented) The method of claim 36, wherein said first set of DNA sequences that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a FATB gene comprises a FAD2 intron.

85. (Previously Presented) The method of claim 36, wherein said first set of DNA sequences that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a FATB gene comprises a FAD2 intron and a FATB UTR.

86. (Previously Presented) The method of claim 36, wherein said first set of DNA sequences that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a FATB gene comprises a FATB UTR.

87. (Previously Presented) The method of claim 36, wherein said transforming a plant cell with a recombinant nucleic acid molecule comprises cotransforming a first recombinant nucleic acid molecule comprising a DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a second recombinant nucleic acid molecule comprising a DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FATB gene.

88. (Previously Presented) The method of claim 36, wherein said transforming comprises sequentially transforming a first recombinant nucleic acid molecule comprising a DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a second recombinant nucleic acid molecule comprising a DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FATB gene.

89. (Previously Presented) The method of claim 36, wherein said transforming comprises a single transformation of one recombinant nucleic acid molecule comprising a first DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FAD2 gene and a second DNA sequence that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a FATB gene.

90. (Previously Presented) The method of claim 36, wherein said first set of DNA sequences comprises a single contiguous FAD2 sequence or a combination of FAD2 sequences.

91. (Previously Presented) The method of claim 36, wherein said first set of DNA sequences comprises a single contiguous FATB sequence or a combination of FATB sequences.

92. (Previously Presented) The method of claim 36, wherein said first set and second set of DNA sequences are located on one or more T-DNA regions, wherein each said T-DNA is flanked by a right border and a left border.

93. (Currently Amended) A method of altering the oil composition of a soybean plant cell comprising:

(A) transforming a plant cell with a recombinant nucleic acid molecule which comprises a first set of DNA sequences that is capable, when expressed in a soybean host cell, of suppressing the endogenous expression of at least a soybean FAD2 gene and a soybean FATB gene,

(B) crossing a plant cell comprising a second set of DNA sequences that is capable, when expressed in a host cell, of increasing the endogenous expression of at least a delta-9 desaturase gene; and

(C) growing said soybean plant cell under conditions wherein transcription of said first set of DNA sequences and said second set of DNA sequences is initiated, whereby said oil composition is altered relative to a soybean plant cell with a similar genetic background but lacking the recombinant nucleic acid molecule.

94. (Currently Amended) A method of producing a transformed soybean plant having seed with a reduced saturated fatty acid content comprising:

(A) transforming a soybean plant cell with a recombinant nucleic acid molecule which comprises a first set of DNA sequences that is capable, when expressed in a host cell, of suppressing the endogenous expression of at least a soybean FAD2 gene and a soybean FATB gene,

(B) crossing a plant cell comprising a second set of DNA sequences that is capable, when expressed in a host cell, of increasing the endogenous expression of at least a delta-9 desaturase gene; and

(C) growing said soybean plant cell under conditions wherein transcription of said first set of DNA sequences and said second set of DNA sequences is initiated, whereby said oil composition is altered relative to a soybean plant cell with a similar genetic background but lacking the recombinant nucleic acid molecule.

95. (New) The method of claim 75, wherein said FAD2 intron is a fragment of a FAD2 intron.

96. (New) The method of claim 76, wherein said FAD2 intron is a fragment of a FAD2 intron.

97. (New) The method of claim 84, wherein said FAD2 intron is a fragment of a FAD2 intron.

98. (New) The method of claim 85, wherein said FAD2 intron is a fragment of a FAD2 intron.